



SEQUENCE LISTING

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The Regents of the University of California

<120> LEAFY COTYLEDON1 Genes and Their Uses

<130> 023070-077630US

<140> US 09/516,052

<141> 2000-03-01

<150> US 09/193,931

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<150> US 09/103,478

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<151> 1998-02-19

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ttccatctgt gtttaattatt agcatttctt ttcctttgtc ttatttgcct ttatttcgta 7020
ggaagaaatc ctttatgnac cccatcttgg ctgagaactt gagatgattt taaatcctca 7080
aaaattattc aatttatgat ttcgaaattg atatacactt tatattttct cctaaaaaac 7140
catattgtac taagaaaagt agaaaaccag actttttaat atgttagatt ttaattgggt 7200
tcttaaagtg ttttagcgtt tnacaccggg tattctccaa aatccaaact ctataattat 7260
agtttttaag tataaattaa tccggttggc ccaattagtg gaccgtttta agagtagaca 7320
cttttttttt tatatatcga ctaccataaa actttaacga ttaatatatt tggataataa 7380
gcgatcggtt tgaggcgctc caattttttt tgtttctttt tatatgagaa atgggtttta 7440
gaaaaactgc aattttgtcc ataaagctag tcagaattcc tgcagcccg gggatccact 7500
agttctagag cggccgccac cgcggtggag ctccaattcg ccctatagtg agtcgtatta 7560

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<210> 5

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA binding
region of HAP3 subunit of CCAAT box-binding factor
(CBF) protein B domain homolog with transcription
activation function

<400> 5

Met Pro Ile Ala Asn Val Ile

1

5

<210> 6

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:subunit
interaction domain of HAP3 subunit of CCAAT
box-binding factor (CBF) protein B domain homolog

<400> 6

Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val

1

5

10

<210> 7

<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:UP primer

<400> 7
ggaattcagc aacaacccaa cccca

25

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:LP primer

<400> 8
gctctagaca tacaacactt ttcctta

27

<210> 9
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:alternative
primer

<400> 9
atgaccagct cagtcatagt agc

23

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:alternative
primer

<400> 10
gccacacatg gtggttgctg ctg

23

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:alternative
primer

<400> 11
gagatagaga ccgatcgtgg ttc

23

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:alternative
primer

<400> 12
tcacttatac tgaccataat ggtc

24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:left border
specific primer

<400> 13
gcatagatgc actcgaaatc agcc

24

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T-DNA left
border specific primer

<400> 14
gcttggtaat aattgtcatt ag

22

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H21 primer

<400> 15
ctaaaaacat ctacggttca

20

<210> 16
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H17 primer

<400> 16
tttgtggttg accgtttggc

20

<210> 17
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA binding
region of HAP3 subunit of CCAAT box-binding factor
(CBF-A) protein yeast homolog

<400> 17
Leu Pro Ile Ala Asn Val Ala
1 5

<210> 18
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:subunit
interaction domain of HAP3 subunit of CCAAT
box-binding factor (CBF-A) protein yeast homolog

<400> 18
Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val
1 5 10

<210> 19
<211> 618
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(618)
<223> LEAFY COTYLEDON1 (LEC1) -Like (L1L)

<400> 19
atg gca gag ggc agt atg cgt cct cca gaa ttc aac cag cct aac aaa 48
Met Ala Glu Gly Ser Met Arg Pro Pro Glu Phe Asn Gln Pro Asn Lys
1 5 10 15

acc agt aat ggt ggt gag gag gag tgc acg gtg agg gag caa gac agg 96
Thr Ser Asn Gly Gly Glu Glu Glu Cys Thr Val Arg Glu Gln Asp Arg

20	25	30	
ttc atg cct att gcc aac gtg ata cgg atc atg cgg agg atc tta cct			144
Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro			
35	40	45	
gct cac gcc aag atc tca gat gac tcc aag gag acg atc caa gag tgt			192
Ala His Ala Lys Ile Ser Asp Asp Ser Lys Glu Thr Ile Gln Glu Cys			
50	55	60	
gtt tcg gag tac atc agc ttc ata aca ggg gag gct aat gag cgg tgc			240
Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys			
65	70	75	80
cag cgg gaa cag cgc aag acc atc act gct gag gac gtc ttg tgg gca			288
Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala			
85	90	95	
atg agc aag ctc ggt ttt gat gac tac atc gaa ccc ctc acg ttg tac			336
Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Leu Tyr			
100	105	110	
ctc cac cgc tac aga gag ttg gaa ggt gaa aga ggg gtt agc tgc agt			384
Leu His Arg Tyr Arg Glu Leu Glu Gly Glu Arg Gly Val Ser Cys Ser			
115	120	125	
gct ggg tcc gtt agt atg acc aac ggc ttg gtg gtc aag agg cct aat			432
Ala Gly Ser Val Ser Met Thr Asn Gly Leu Val Val Lys Arg Pro Asn			
130	135	140	
ggg acc atg acc gag tat gga gcc tac ggg cct gtg cca ggg att cac			480
Gly Thr Met Thr Glu Tyr Gly Ala Tyr Gly Pro Val Pro Gly Ile His			
145	150	155	160
atg gcg cag tac cat tat cgt cat cag aac ggg ttt gtt ttc agt ggt			528
Met Ala Gln Tyr His Tyr Arg His Gln Asn Gly Phe Val Phe Ser Gly			
165	170	175	
aac gaa cct aat tct aag atg agt ggt tca tct tca gga gca agt ggc			576
Asn Glu Pro Asn Ser Lys Met Ser Gly Ser Ser Ser Gly Ala Ser Gly			
180	185	190	
gcc aga gtt gaa gta ttt ccg act caa caa cat aag tac tga			618
Ala Arg Val Glu Val Phe Pro Thr Gln Gln His Lys Tyr			
195	200	205	

<210> 20

<211> 205

<212> PRT

<213> Arabidopsis thaliana

<400> 20

Met Ala Glu Gly Ser Met Arg Pro Pro Glu Phe Asn Gln Pro Asn Lys

1 5 10 15
Thr Ser Asn Gly Gly Glu Glu Glu Cys Thr Val Arg Glu Gln Asp Arg

20

25

30

Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro
 35 40 45
 Ala His Ala Lys Ile Ser Asp Ser Lys Glu Thr Ile Gln Glu Cys
 50 55 60
 Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys
 65 70 75 80
 Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala
 85 90 95
 Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Leu Tyr
 100 105 110
 Leu His Arg Tyr Arg Glu Leu Glu Gly Glu Arg Gly Val Ser Cys Ser
 115 120 125
 Ala Gly Ser Val Ser Met Thr Asn Gly Leu Val Val Lys Arg Pro Asn
 130 135 140
 Gly Thr Met Thr Glu Tyr Gly Ala Tyr Gly Pro Val Pro Gly Ile His
 145 150 155 160
 Met Ala Gln Tyr His Tyr Arg His Gln Asn Gly Phe Val Phe Ser Gly
 165 170 175
 Asn Glu Pro Asn Ser Lys Met Ser Gly Ser Ser Ser Gly Ala Ser Gly
 180 185 190
 Ala Arg Val Glu Val Phe Pro Thr Gln Gln His Lys Tyr
 195 200 205

<210> 21
 <211> 987
 <212> DNA
 <213> Phaseolus coccineus

<220>
 <223> clone pCEP112 insert

<220>
 <221> CDS
 <222> (66)..(716)
 <223> scarlet runner bean (SRB) LEC1 ortholog

<400> 21
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 tcacc atg gaa agt gga ggc ttt cat ggc tac cgc aag ctc ccc aac acc 110
 Met Glu Ser Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr
 1 5 10 15
 acc tct cct ggg ttg aag ctg tca gtg tca gac atg aac aac gtg aac 158
 Thr Ser Pro Gly Leu Lys Leu Ser Val Ser Asp Met Asn Asn Val Asn
 20 25 30
 acg agt agg cag gta gca gga gac aac aac cac aca gcg gat gag agc 206
 Thr Ser Arg Gln Val Ala Gly Asp Asn Asn His Thr Ala Asp Glu Ser
 35 40 45
 aac gaa tgc act gtg agg gag caa gac cgt ttc atg cca att gca aat 254
 Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe Met Pro Ile Ala Asn
 50 55 60

gtg atc agg atc atg cga aag att ctt cct cca cat gcc aag atc tca 302
 Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro His Ala Lys Ile Ser
 65 70 75
 ggt gat gcc aaa gaa aca att caa gag tgt gtg tct gag tac atc agc 350
 Gly Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser
 80 85 90 95
 ttt atc acc gga gag gca aac gag cgt tgc cag agg gaa caa cgc aag 398
 Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys
 100 105 110
 acc ata act gct gag gac gtg ctt tgg gcc atg agc aag ctt gga ttt 446
 Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Lys Leu Gly Phe
 115 120 125
 gat gat tac atg gag cca ctg acc atg tac ctt cac agg tat cgt gag 494
 Asp Asp Tyr Met Glu Pro Leu Thr Met Tyr Leu His Arg Tyr Arg Glu
 130 135 140
 ctt gag ggt gac cga acc tcc atg aga ggt gaa tca ttg ggg aag agg 542
 Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu Ser Leu Gly Lys Arg
 145 150 155
 act att gaa tac gcc cct atg ggt gtt ggc gtt gct act gct ttt gtg 590
 Thr Ile Glu Tyr Ala Pro Met Gly Val Gly Val Ala Thr Ala Phe Val
 160 165 170 175
 cca cca cag ttt cac cca aat gga tac tat ggt cct gcc atg gga gct 638
 Pro Pro Gln Phe His Pro Asn Gly Tyr Tyr Gly Pro Ala Met Gly Ala
 180 185 190
 tac gtt gcg cca cca aat gct gcg tcc tct cat cac cat gga atg cca 686
 Tyr Val Ala Pro Pro Asn Ala Ala Ser Ser His His His Gly Met Pro
 195 200 205
 aat act gaa ccg aat gct cgc tcc atg tga attgatgatg atgaggagga 736
 Asn Thr Glu Pro Asn Ala Arg Ser Met
 210 215
 ggaggaggaa gacgacgagt gttgagttag tagaagaaga atactttaat taattagctt 796
 aactctcggg aattagagta ctgttggttga gggtagctag taaactttat aattaagggg 856
 atggatggga ttaaggagtt ctgatattcc taatcctaata caggcctatg ttaatttatg 916
 taataactct gcttatgttt ttggattttc tgatgttggt ccaaaaaaaaa aaaaaaaaaa 976
 aaaaaaaaa a 987

<210> 22
 <211> 216
 <212> PRT
 <213> Phaseolus coccineus
 <223> clone pPCEP112 insert

<400> 22

Met Glu Ser Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr
1 5 10 15
Ser Pro Gly Leu Lys Leu Ser Val Ser Asp Met Asn Asn Val Asn Thr
20 25 30
Ser Arg Gln Val Ala Gly Asp Asn Asn His Thr Ala Asp Glu Ser Asn
35 40 45
Glu Cys Thr Val Arg Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val
50 55 60
Ile Arg Ile Met Arg Lys Ile Leu Pro Pro His Ala Lys Ile Ser Gly
65 70 75 80
Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe
85 90 95
Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr
100 105 110
Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp
115 120 125
Asp Tyr Met Glu Pro Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu
130 135 140
Glu Gly Asp Arg Thr Ser Met Arg Gly Glu Ser Leu Gly Lys Arg Thr
145 150 155 160
Ile Glu Tyr Ala Pro Met Gly Val Gly Val Ala Thr Ala Phe Val Pro
165 170 175
Pro Gln Phe His Pro Asn Gly Tyr Tyr Gly Pro Ala Met Gly Ala Tyr
180 185 190
Val Ala Pro Pro Asn Ala Ala Ser Ser His His His Gly Met Pro Asn
195 200 205
Thr Glu Pro Asn Ala Arg Ser Met
210 215

<210> 23

<211> 2000

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> promoter

<222> (1)..(2000)

<223> 5' untranslated region

<400> 23

tgggttttca aaggaagagg atgattctct tctctctctt caaatggagt ttcaagctcg 60
aaatcgcac tcttgggatg gtctctctct caggtataaa tctcaccatt aaaaatgtga 120
gctttttgtt caactttgga tctgttactg tgaaaagtgt ttactttttt tctgtattat 180
taagagtcta attttttttc acgtttatta gaagcttggt tggtagagac ctctaaaca 240
cattctcttc ctcttgatat atttgagctt tgcggtatca tttgattcta gattgggtga 300
ctggtgcatc actgaacact ctcagcttaa agcattaaac tttgcagata tcaatcagat 360
tggtgtgccg tcattacaag cttttacagt gttggtttat accacttcta agcagtgttt 420
gtctatatat tctgcggaac ttttggatta ttagttctta gatagtgtaa ccatgttgga 480
agctttgagt ttttgataag tactttccaa tttttgattt tgcagctcct ctggtgatag 540
cagcgatagt gactcatctc cagacgttcg caagaccgtc acgggtaaaa gaaagcggga 600
aacaagggtg aagctggagc atttcttgga gaagcttggt gggagtatga tgaagcggca 660
ggagaagatg cataatcagt tgattaatgt gatggagaag atggaagtgg agagaatacg 720
ccgtgaggaa gcttggaggc aacaggaaac cgagaggatg acacagaatg aagaagcacg 780
gaagcaagag atggcacgca acttgtctct catctctttc atcagaagtg ttactgggtga 840

cgagatcgag	atccctaacc	agtgtgaatt	cccgcaccca	ctccagcaga	ttcttccgga	900
acaatgtaaa	gacgagaaat	gtgaatccgc	tcagagagaa	agagagataa	agtttaggta	960
ctcaagcggc	agtggcagca	gtggtagaag	gtggccgcaa	gaggaagtgc	agggcattgat	1020
aagttcgaga	agcgatgtgg	aagagaagac	ggggatcaac	aagggagcga	tttgggatga	1080
gatatcgaca	agaatgaaaag	aaagagggta	cgaaagatct	gcgaaaaagt	gtaaggagaa	1140
gtgggagaac	atgaacaagt	actataggag	agtgcaggaa	ggtgggcaga	aacagcctga	1200
gcacagcaag	actcgctcat	actttgagaa	acttggaaat	ttttacaaga	ccatttcctc	1260
gggagagagg	gaaaaatgag	tgaaagattt	taaatttagg	tgtttttggc	acgcaaaacg	1320
ggagaacttg	tagatgatta	cctcgagttt	aatttttata	tctttggtgt	agttttataat	1380
ttaaaactct	acggctctgt	attttagtaa	ggttcgaata	aaaaagacaa	atagcttggg	1440
gtgattggga	ttttgtaacg	gctaaggagg	acgaggagaa	ggatcctcgg	tcacatcgat	1500
tatggctgcc	acgttgttga	acttgtgagg	tctgaaatta	caaagtctga	cacttgccaa	1560
cactattagc	tttattccaa	ttactctttc	ttctctctca	ttccattctc	ttcttcaa	1620
gcttcttaat	ttcgggcatt	ggttattatt	atttataggg	atattcacia	acacaaaagt	1680
cgtgtattta	gaacaagaaa	gatatggaac	gtggaggctt	ccatggctac	cgcaagctgt	1740
ccgtgaacaa	caccactcct	tctccaccag	gtagtgccat	tctctatacc	ccctcttttc	1800
acaggctctc	ttcatttcag	ttgcatgcga	aaccattctc	tgcaatccct	ccattgtcat	1860
gtctgtactc	ttttcatgac	gaacagttaa	tgaaatagct	tttcaatctt	ataaaccgcg	1920
catgcagacg	tcacgaagc	cattatgcac	taaaacttcc	atttttctta	tttttgtag	1980
gattagcagc	gaattttctg					2000

<210> 24
 <211> 1000
 <212> DNA
 <213> Arabidopsis thaliana
 <220>
 <221> promoter
 <222> (1)..(1000)
 <223> 3' untranslated region

<400> 24						
gaacaatggc	taataacata	gacagctgac	agagtcataa	ctgttagtag	gtgcaagctg	60
tagcttatga	attcaagttt	aagcgaaaac	aatgctgctt	tttctttgtt	tattatctat	120
ctagttgaaa	gaacattgtg	tttttcatct	gatctgtctt	gtggtaaagt	atgtcaataa	180
agcattagtt	ttgcaaacgg	catgcatgtg	atattacaaa	attcacgggtg	aattcgtaat	240
gcgctcttgg	tcaaaataga	aagagactaa	acattccaga	tttcaattct	cagctacaga	300
aatgagtgtt	taacggatac	agaaacaact	ctcacaatct	tcattcattt	catttagcta	360
ctactttcca	aaggaacttc	aacgcatacc	tttttctctt	ccagaagatc	atgtttgtct	420
gcactctcgt	ttgcctcagt	atctttctcc	tgatgctctt	cagatatatg	ttccaatttc	480
gaacaatcaa	caggatcaag	tccggttctt	ttcctctgag	gaatcacagt	gaagaaggct	540
gttttccagt	ccctagtctc	cagaaaacttg	acgagtatct	ccaaaacttg	gttcacagtg	600
agaacctaaa	tcaataaaaa	ccacaaatct	tacattaaca	aagtacataa	agtagagggt	660
ttttgtgttg	tgcccaatga	gacaagaatt	gaagtggcca	tttagttacc	tgagaacttg	720
acattttcat	atactctcct	atgggaagct	tagctgtttt	aatgccttgt	tcttgagcct	780
tggtcatggg	gatccctttg	aaccggtttc	gatccactaa	gccaccgata	atgtagatat	840
gcttaggggc	aagatcatcc	aaaacagttt	cagaatcagc	cgtaagatac	accaaattat	900
ctttctgac	agccatggct	tcaatgtaac	acctactttc	cttttcaatg	aaccatttct	960
caaaaccagg	aagcttgtca	agctcagtag	tcacttctcc			1000

<210> 25
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer of third
 set

<400> 25
 aggatccatg gaacgtggag gcttccat 28

<210> 26
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer of third
 set

<400> 26
 atctagatca gtacttatgt tggtgagtcg 30

<210> 27
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:forward primer
 BAMMNJ7-5

<400> 27
 aggatccatg gaacgtggag gcttccat 28

<210> 28
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:reverse primer
 3-MNJ7XBA

<400> 28
 atctagatca gtacttatgt tggtgagtcg 30

<210> 29
 <211> 90
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> DOMAIN
 <222> (1)..(90)
 <223> LEC1 HAP3 subunit of CCAAT box-binding factor
 (CBF) protein B domain homolog

20 25 30
 Cys Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu
 35 40 45
 Ala Ser Glu Arg Cys His Gln Glu Lys Arg Lys Thr Ile Asn Gly Glu
 50 55 60
 Asp Ile Leu Phe Ala Met Ser Thr Leu Gly Phe Gln Ser Tyr Val Glu
 65 70 75 80
 Pro Leu Lys Leu Tyr Leu Gln Lys Phe Arg
 85 90

<210> 32
 <211> 90
 <212> PRT
 <213> Petromyzontidae gen. sp.

<220>
 <221> DOMAIN
 <222> (1)..(90)
 <223> lamprey HAP3 subunit of CCAAT box-binding factor
 (CBF) protein B domain homolog

<400> 32
 Arg Glu Gln Asp Ile Tyr Leu Pro Ile Ala Asn Val Ala Arg Ile Met
 1 5 10 15
 Lys Thr Ser Ile Pro Ser Ser Gly Lys Ile Ala Lys Asp Ala Lys Glu
 20 25 30
 Cys Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu
 35 40 45
 Ala Ser Glu Arg Cys His Gln Glu Lys Arg Lys Thr Ile Asn Gly Glu
 50 55 60
 Asp Ile Leu Phe Ala Met Ser Thr Leu Gly Phe Gln Ser Tyr Val Glu
 65 70 75 80
 Pro Leu Lys Gln Tyr Leu Gln Lys Tyr Arg
 85 90

<210> 33
 <211> 57
 <212> PRT
 <213> Xenopus laevis

<220>
 <221> DOMAIN
 <222> (1)..(57)
 <223> Xenopus HAP3 subunit of CCAAT box-binding factor
 (CBF) protein B domain homolog

<400> 33
 Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala
 1 5 10 15
 Ser Glu Arg Cys His Gln Glu Lys Arg Lys Thr Ile Asn Gly Glu Asp
 20 25 30
 Ile Leu Phe Ala Met Ser Thr Leu Gly Phe Gln Ser Tyr Val Glu Pro
 35 40 45
 Leu Lys Leu Tyr Leu Gln Lys Phe Arg
 50 55

<210> 34
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (1)..(90)
 <223> human HAP3 subunit of CCAAT Box-binding factor
 (CBF) protein B domain homolog

<400> 34
 Arg Glu Gln Asp Ile Tyr Leu Pro Ile Ala Asn Val Ala Arg Ile Met
 1 5 10 15
 Lys Asn Ala Ile Pro Gln Thr Gly Lys Ile Ala Lys Asp Ala Lys Glu
 20 25 30
 Cys Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu
 35 40 45
 Ala Ser Glu Arg Cys His Gln Glu Lys Arg Lys Thr Ile Asn Gly Glu
 50 55 60
 Asp Ile Leu Phe Ala Met Ser Thr Leu Gly Phe Gln Ser Tyr Val Glu
 65 70 75 80
 Pro Leu Lys Leu Tyr Leu Gln Lys Phe Arg
 85 90

<210> 35
 <211> 90
 <212> PRT
 <213> Mus musculus and Rattus norvegicus

<220>
 <221> DOMAIN
 <222> (1)..(90)
 <223> mouse/rat HAP3 subunit of CCAAT box-binding factor
 (CBF) protein B domain homolog

<400> 35
 Arg Glu Gln Asp Ile Tyr Leu Pro Ile Ala Asn Val Ala Arg Ile Met
 1 5 10 15
 Lys Asn Ala Ile Pro Gln Thr Gly Lys Ile Ala Lys Asp Ala Lys Glu
 20 25 30
 Cys Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu
 35 40 45
 Ala Ser Glu Arg Cys His Gln Glu Lys Arg Lys Thr Ile Asn Gly Glu
 50 55 60
 Asp Ile Leu Phe Ala Met Ser Thr Leu Gly Phe Gln Ser Tyr Val Glu
 65 70 75 80
 Pro Leu Lys Leu Tyr Leu Gln Lys Phe Arg
 85 90

<210> 36
 <211> 90
 <212> PRT

<213> *Emericella nidulans*

<220>

<221> DOMAIN

<222> (1)..(90)

<223> *E. nidulans* HAP3 subunit of CCAAT box-binding factor (CBF) protein B domain homolog

<400> 36

Lys	Glu	Gln	Asp	Arg	Trp	Leu	Pro	Ile	Ala	Asn	Val	Ala	Arg	Ile	Met
1				5					10					15	
Lys	Leu	Ala	Leu	Pro	Glu	Asn	Ala	Lys	Ile	Ala	Lys	Glu	Ala	Lys	Glu
		20					25					30			
Cys	Met	Gln	Glu	Cys	Val	Ser	Glu	Phe	Ile	Ser	Phe	Ile	Thr	Ser	Glu
	35					40				45					
Ala	Ser	Glu	Lys	Cys	Gln	Gln	Glu	Lys	Arg	Lys	Thr	Val	Asn	Gly	Glu
	50				55					60					
Asp	Ile	Leu	Phe	Ala	Met	Thr	Ser	Leu	Gly	Phe	Glu	Asn	Tyr	Ala	Glu
65				70					75						80
Ala	Leu	Lys	Ile	Tyr	Leu	Ser	Lys	Tyr	Arg						
			85					90							

<210> 37

<211> 85

<212> PRT

<213> *Schizosaccharomyces pombe*

<220>

<221> DOMAIN

<222> (1)..(85)

<223> *S. pombe* HAP3 subunit of CCAAT box-binding factor (CBF) protein B domain homolog

<400> 37

Leu	Leu	Pro	Ile	Ala	Asn	Val	Ala	Arg	Ile	Met	Lys	Ser	Ala	Leu	Pro
1				5				10						15	
Glu	Asn	Ala	Lys	Ile	Ser	Lys	Glu	Ala	Lys	Asp	Cys	Val	Gln	Asp	Cys
		20					25					30			
Val	Ser	Glu	Phe	Ile	Ser	Phe	Val	Thr	Gly	Glu	Ala	Ser	Glu	Gln	Cys
	35				40					45					
Thr	Gln	Glu	Lys	Arg	Lys	Thr	Ile	Thr	Gly	Glu	Asp	Val	Leu	Leu	Ala
	50				55				60						
Leu	Asn	Thr	Leu	Gly	Phe	Glu	Asn	Tyr	Ala	Glu	Val	Leu	Lys	Ile	Ser
65				70				75							80
Leu	Thr	Lys	Tyr	Arg											
			85												

<210> 38

<211> 90

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> DOMAIN

<222> (1)..(90)

<223> *S. cerevisiae* HAP3 subunit of CCAAT box-binding factor (CBF) protein B domain homolog

<400> 38

Arg	Glu	Gln	Asp	Arg	Trp	Leu	Pro	Ile	Asn	Asn	Val	Ala	Arg	Leu	Met
1				5					10					15	
Lys	Asn	Thr	Leu	Pro	Pro	Ser	Ala	Lys	Val	Ser	Lys	Asp	Ala	Lys	Glu
			20					25					30		
Cys	Met	Gln	Glu	Cys	Val	Ser	Glu	Leu	Ile	Ser	Phe	Val	Thr	Ser	Glu
		35					40					45			
Ala	Ser	Asp	Arg	Cys	Ala	Ala	Asp	Lys	Arg	Lys	Thr	Ile	Asn	Gly	Glu
	50					55					60				
Asp	Ile	Leu	Ile	Ser	Leu	His	Ala	Leu	Gly	Phe	Glu	Asn	Tyr	Ala	Glu
65					70					75					80
Val	Leu	Lys	Ile	Tyr	Leu	Ala	Lys	Tyr	Arg						
				85					90						

<210> 39

<211> 90

<212> PRT

<213> *Kluyveromyces lactis*

<220>

<221> DOMAIN

<222> (1)..(90)

<223> *K. lactis* HAP3 subunit of CCAAT box-binding factor (CBF) protein B domain homolog

<400> 39

Ala	Glu	Gln	Asp	Arg	Trp	Leu	Pro	Ile	Asn	Asn	Val	Ala	Arg	Leu	Met
1				5					10					15	
Lys	Asn	Thr	Leu	Pro	Ala	Thr	Thr	Lys	Val	Ser	Lys	Asp	Ala	Lys	Glu
			20					25					30		
Cys	Met	Gln	Glu	Cys	Val	Ser	Glu	Phe	Ile	Ser	Phe	Val	Thr	Ser	Glu
		35					40					45			
Ala	Cys	Asp	Arg	Cys	Thr	Ser	Gly	Lys	Arg	Lys	Thr	Ile	Asn	Gly	Glu
	50					55					60				
Asp	Ile	Leu	Leu	Ser	Leu	His	Ala	Leu	Gly	Phe	Glu	Asn	Tyr	Ala	Glu
65					70					75					80
Val	Leu	Lys	Ile	Tyr	Leu	Ala	Lys	Tyr	Arg						
				85					90						